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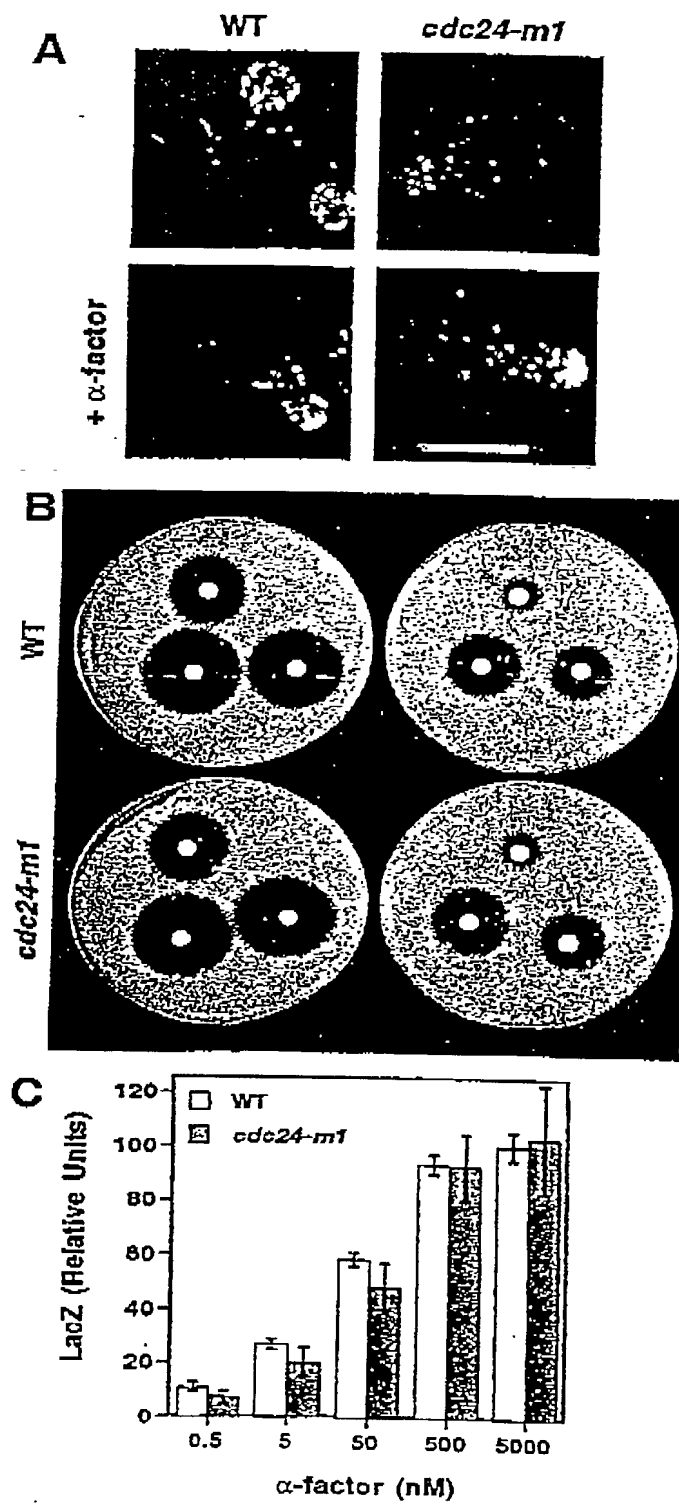


FIG. 1

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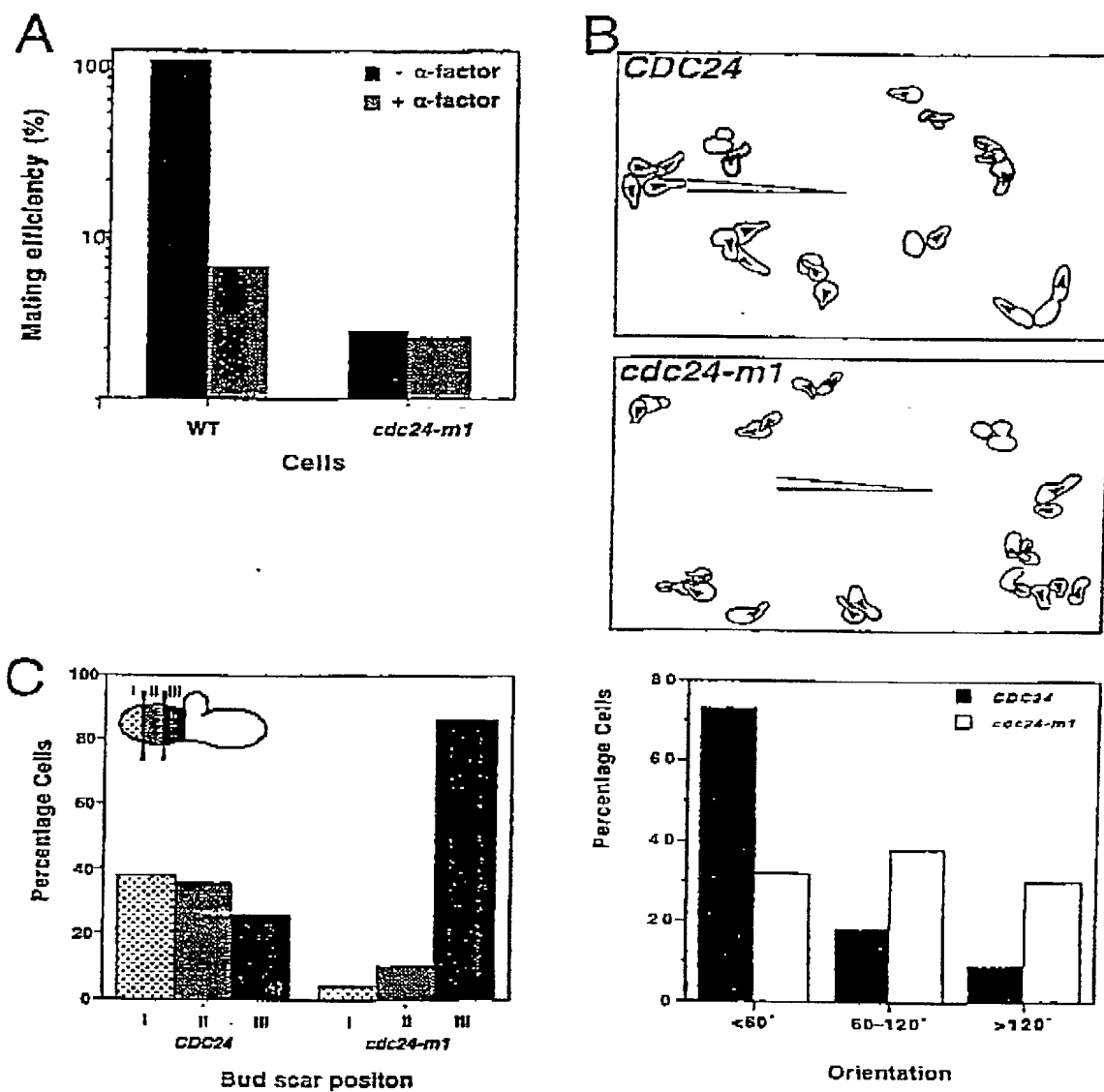


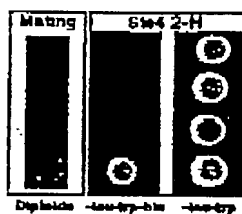
FIG. 2

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A

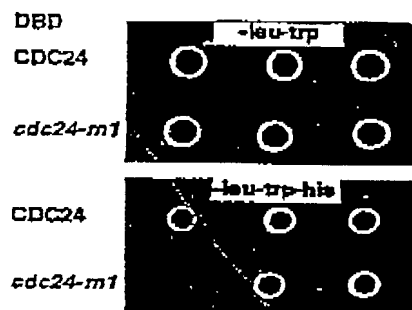
Cdc24-m1	QFKLPVIAFDRLRVCKKSI
Cdc24-m2	QFKLPVIASGDLRVCKKSI
Cdc24-m3	QFKLPVIAFDRLRVCKKSI
Cdc24 Sc	181 QFKLPVIASGDLRVCKKSI 189

Dhl Hu	335 QYEFDVILSPDLKVGKTI 403

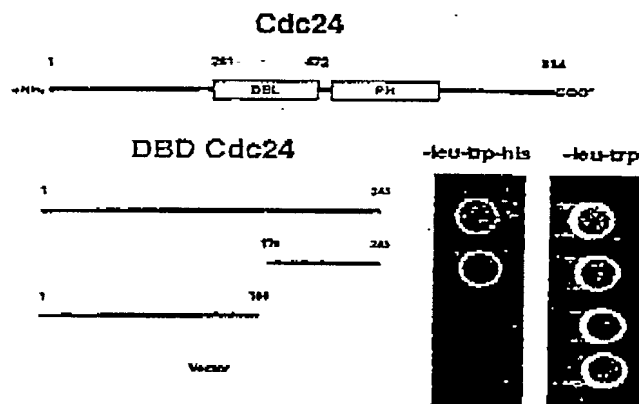


B

AD STE4 CDC42 BEM1



C



D



FIG. 3

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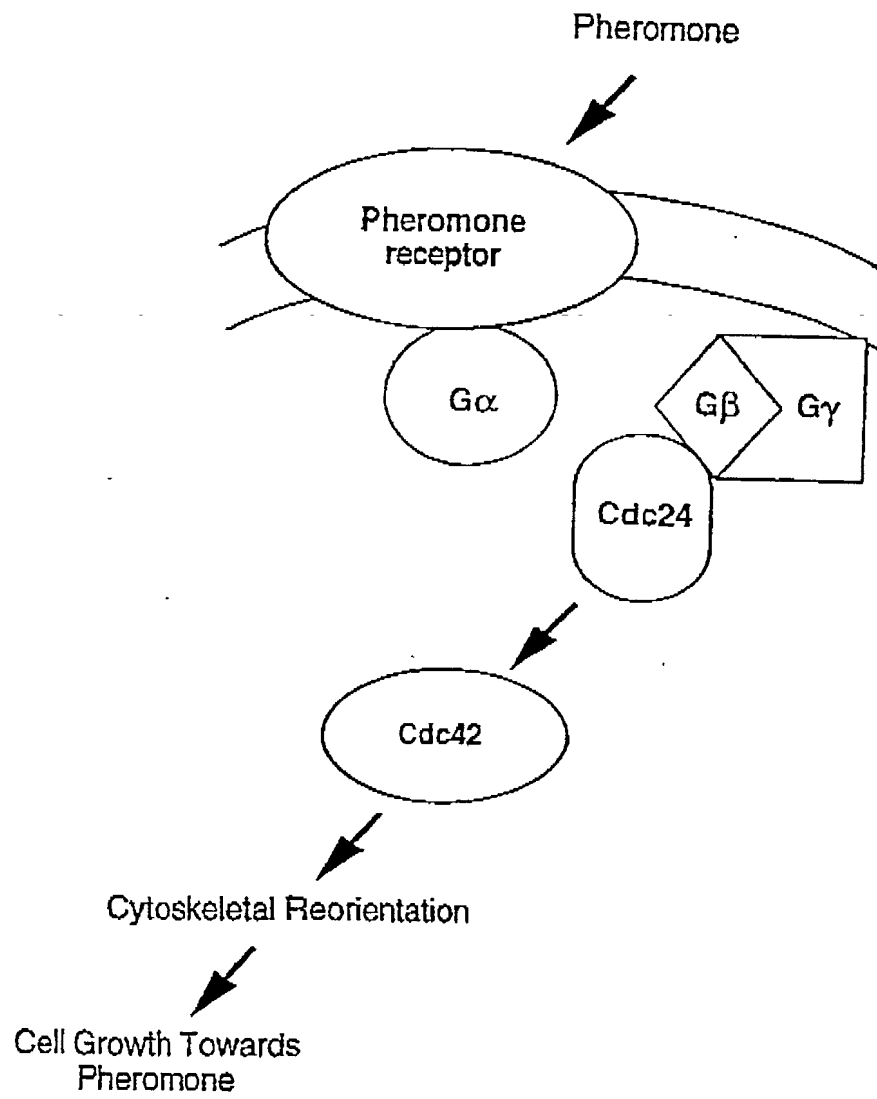


FIG. 4

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Figure 5

5	2113/1	ATG GAA CAT CCA CCA GCA GCT CTC AGA ACA	2143/11	TTT TCA ACC CAA TCA ACT TCA TCT TTG AAT
	2173/21	M E H P P A A L R T	2203/31	F S T Q S T S S L N
10	TCA GTA AGT ACT GTT TCG TCT TCA AGA ATT	GTT TCT CTG GGC CCA GTC AAT ATA AAC AAT		S V S T V S S S R I V S S G P V N I N N
	2233/41	TTC AAT AAA CCA AGT ACT CCC AAA GAC CAT	2263/51	TTA TTC TAT CGA TGT GAA TCA CTA AAA CGA
15	F N K P S T P K D H	L F Y R C E S L K R	2323/71	AAA CTA CAA AAA ATC CCT GGC ATG GAA CCA
	2293/61	K L Q K I P G M E P	2383/91	F L N Q A F N Q A E
	2353/81	CAA CTC AGT GAA CAA CAA GCA TTG GCT TTG	2443/111	GCA CAG GAA AGA AGC AAT GGA AAT GGA CAT
20	Q L S E Q Q A L A L	A Q E R S N G N G H		AGT AAT GGC AAA CGT CAT CAA TCA TTA GAC
	2413/101	S N G K R H Q S L D	2503/131	G A M N R L S V G S
25	GAT AGT AGT TCG ATC CAA GGT TCA TTG ACA	CGA ATG GCC ACC AAT GCG TCA ACG TCA TCT		D S S S I Q G S L T R M A T N A S T S S
	2533/141	TTA ATC AGT GGT ATG CCA AAC AAC AAC ACT	2563/151	TTA TTT ACG TTT ACT GCA GGG GTT TTA CCA
30	L I S G M P N N N T	L F T F T A G V L P	2623/171	CTT TGG AAA TTG TTC CAA CAA GGG GCC CCC
	2593/161	A N I S V D P A T H	2683/191	GAT TCC CAA ATA CCA GTT GTC AGT TCT GAT
35	TTT TGT GTT CTT ATC AAT CAT ATC CTT CCT	D S Q I P V V S S D		2713/201
	GAC TTG AGA ATT TGC AAA AAA TCA GTA TAT	GAC TTT TTA ATT GCC GTC AAG ACA CAA TTG		D L R I C K K S V Y D F L I A V K T Q L
40	AAT TTT GAT GAC GAG AAT ATG TTC ACT ATA	TCC AAT GTT TTC TCC GAC AAT GCC CAA GAT		2773/221
	N F D D E N M F T I	S N V F S D N A Q D		2833/241
	TTA ATC AAG ATT ATT GAT GTC ATT AAT AAA	CTA CTT GCT GAG TAC TCA GAT GCT AGT GAC		L I K I I D V I N K L L A E Y S D A S D
45	2893/261	CTG GGT GGT GGC GAT GAA GAT GTA AAT ATG	GAT GTT CAA ATT ACC GAT GAA AGA TCA AAA	
	2953/281	S G G G D E D V N M D V Q I T D E R S K		2983/291
50	GTT TTC CGA GAA ATT ATC GAA ACA GAA AGA	AAA TAT GTT CAA GAC TTG GAA CTA ATG TGT		V F R E I I E T E R K Y V Q D L E L M C
	3013/301	AAA TAC CGT CAA GAT CTA ATT GAA GCC GAA	AAT TTG TCT TCA GAA CAA ATT CAC TTG TTA	
	3073/321	K Y R Q D L I E A E N L S S E Q I H L L		3103/331
55	TTC CCA AAT TTA AAT GAG ATT ATT GAT TTT	CAA AGA CGA TTC CTC AAT GGG TTA GAA TGT		F P N L N E I I D F Q R R F L N G L E C
	3133/341	AAC ATC AAT GTA CCT ATT AGA TAT CAA AGA	ATT GGA TCA GTA TTT ATT CAT GCT TCT TTG	
60	N I N V P I R Y Q R	I G S V F I H A S L		3193/361
	GGC CCT TTC AAT GCT TAT GAA CCT TGG ACT	ATA GGA CAA TTG ACG GCG ATT GAT TTG ATC		G P F N A Y E P W T I G Q L T A I D L I
	3253/381	AAC AAA GAA GCT GCT AAT TTG AAA AAA TCG	TCA AGT CTA CTT GAT CCT GGG TTT GAA CTT	
65	N K E A A N L K K S	S S L L D P G F E L		3313/401
	CAA TCG TAT ATA TTA AAG CCG ATC CAA AGA	TTG TGT AAA TAC CCA CTT TTG TTG AAA GAG		Q S Y I L K P I Q R L C K Y P L L L K E
	3373/421	TTA ATC AAA ACA TCA CCA GAA TAT TCA AAA	CAG GAC CCC CAT GGC AGC TCG TCA TCG ACA	
70	L I K T S P E Y S K	Q D P H G S S S S T		3433/441
	TCA TTC AAT GAA TTA TTG GTG GCT AAA ACT	GCA ATG AAA GAA TTG GCA AAT CAA GTC AAT		S F N E L L V A K T A M K E L A N Q V N

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3493/461
 GAG CGC CAA AGA CGA GCA GAA AAT ATC GAA
 E A Q R R A E N I E
 3553/481
 AAT TGG CGT GGG TTT AAT TTG GAT GCT CAA
 N W R G F N L D A Q
 3613/501
 GTT AAA GAT GCT GAA AAT GAA AAG GAA TAC
 V K D A E N E K E Y
 3673/521
 TTT TTC ACA GAA ATT GAT GAT ACC AAA AAA
 F F T E I D D T K K
 3733/541
 TCG ACA AGA AAG AGA TCA ACT TCA TCA AAT
 S T R K R S T S S N
 3793/561
 TCA ATA AAC AAT TCC CGA AAG GAT AAC ACA
 S I N N S R K D N T
 3853/581
 ATA TCG GAG ATT TAT AAC ATT TCC GCA CCA
 I S E I Y N I S A P
 3913/601
 TGG TCA GGT AGA AAG GAA AGC GGC TCA TTC
 W S G R K E S G S F
 3973/621
 AAC CAA TGG GAA AAG TGT TTA CGT GAT TTG
 N Q W E K C L R D L
 4033/641
 AAG AAG TTA CGT GAT TCC GAC CTG TCA TTT
 K K L R D S D S S F
 4093/661
 ACG GGT ATT AGT ACG TCA CCA GTC AAT CAA
 T G I S T S P V N Q
 4153/681
 GGC TCT CAC AGT TCC CGC CAT CAC TCA TCG
 G S H S S R H H S S
 4213/701
 AGA GTT AAA TCT GGT GAT TTG AGT AGA ATA
 R V K S G D L S R I
 4273/721
 AGT AAC AAC TTG AAT GGG TCA CCA AAT ACC
 S N N L N G S P N T
 4333/741
 ACC AAA ACA ATT CCA ACA TTT GAC GTT GCA
 T K T I P T F D V A
 4393/761
 TCA GAG CCA TTG ATT GTC AAT GCA CAA ATT
 S E P L I V N A Q I
 4453/781
 TCC CAG ATT ATC ACT TCG AAC TTG GTG GCA
 S Q I I T S N L V A
 4513/801
 AAA GAC GAC GAA GGA GAC TTT GTG AAT TTG
 K D D E G D F V N L
 4573/821
 GAT ATG TTA ACC AGT GAA GAC TTT TAC CAA
 D M L T S E D F Y Q
 4633/841
 GTG TGG GTT TCT TGA
 V W V S *

3523/471
 CAT TTG GAA AAA CTA AAA GAA AGA GTA GGT
 H L E K L K E R V G
 3583/491
 GGA GAA CTA TTA TTC CAC GGA CAA GTT GGG
 G E L L F H G Q V G
 3643/511
 GTT GCT TAT CTT TTT GAA AAA ATC GTA TTT
 V A Y L F E K I V F
 3703/531
 TCT GAT AAA CAG GAA AAG AAG AGC AAG TTT
 S D K Q E K K S K F
 3763/551
 CTT AGT TCA TCG ACT ACT AAT TTG TTG GAA
 L S S S T T N L L E
 3823/571
 TTG CCA TTG GAA TTA AAG GGA AGA GTT TAT
 L P L E L K G R V Y
 3883/591
 AAC ACT CCT GGC TCA ACT CTA ATC ATC TCA
 N T P G S T L I I S
 3943/611
 ACT TTG AGA TAT CGT AGT GAA GAA GCC AGA
 T L R Y R S E E A R
 4003/631
 AAG ACT AAT GAA ATG AAT AAA CAA ATT CAT
 K T N E M N K Q I H
 4063/651
 AAT ACT GAT GAC TCT GCC ATA TAT GAT TAC
 N T D D S A I Y D Y
 4123/671
 TCA ACT CAA CAA CAA TAC TAT GAT CAT CGG
 S T Q Q Q Y Y D H R
 4183/691
 TCA TCC ACT TTG AGT ATG ATG AAG AAT AAT
 S S T L S M M K N N
 4243/711
 TCT TCA ACT TCA ACA ACA TTA GAT TCT TTC
 S S T S T T L D S F
 4303/731
 ACT AAT CCA TCT TTG ATG TCT TCA GAT GCC
 T N P S L M S S D A
 4363/751
 ATT AAA TTG CTT TAC AAA TCG ACA GAA TTG
 I K L L Y K S T E L
 4423/771
 GAG TAT AAT GAC CTT TTA CAG AAA ATT ATC
 E Y N D L L Q K I I
 4483/791
 GAT GAT GTC AAT ATT AGT CGA TTG AGA TAT
 D D V N I S R L R Y
 4543/811
 AAT TCA GAT GAT GAT TGG GGG TTA GTG CTT
 N S D D D W G L V L
 4603/831
 ACA TCA AGC AAT GAA AAA CGA CTG GTG ACA
 T S S N E K R S V T

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Figure 6

5 Blastp line up of S.c. Cdc24p and C.a. Cdc24p

S.c. Cdc24p: 1 MAIQ---TR-FA 8
M R F+

10 C.a. Cdc24p: 1 MEHPPAALRTFSTQ 14

S.c. Cdc24p: 9 SGTSLSDLKPKPSATSISIPMQNV--MNKPVTEQDSLPHICANIRKRLEVLPOLKPFLLQ 66
S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL

15 C.a. Cdc24p: 15 STSSLNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEPFLNQ 74

S.c. Cdc24p: 67 AYQSSEVLSEKQSLLLSOKQHQLLKSNGANRDSLDAP--TLRSSISISTATSLMSMEG 123
A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M

20 C.a. Cdc24p: 75 AFNQAEQLSEQQALALAQERSNGNGHSGNGKRHQSLDGAMNRLSVGSDSSSIQGSILTRMAT 134

S.c. Cdc24p: 124 ISYTSNPSATPNMEDTLTLTFSMGILPITMDCDPVTQLSOLFQOGAPLCILFNSVKPFQK 183
+ T+S S PN +TL TF+ G+LP + DP T L +LFQOGAP C+L N + P +

25 C.a. Cdc24p: 135 NASTSSLISGMPN--NNTLFTFTAGVLPANISVDPATHLWKLFFQOGAPFCVLINHLPSQ 193

S.c. Cdc24p: 184 LPVIASDDLKVKCKSIYDFILGCKKHFAFNDEELFTISDVFNSTEQLVKVEVETLMN 243
+PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+

30 C.a. Cdc24p: 194 IPVVSSDDLRIKCKSVYDFLIAVKTQLNFDDENMFTISNVFSDNAQDLIKIDVINKLLA 253

S.c. Cdc24p: 244 SSPTIFPSKSKTQQIMNAENQHRHQPPQSSKKHNEYVKIIEKFVATERKYVHDLEILDKY 303
S + + + +E K+ +E + TERKYV DLE++ KY

35 C.a. Cdc24p: 254 EYSDASDSGGGDEDV-----NMDVQITDERSKVFREIETERKYVDLELMCKY 302

S.c. Cdc24p: 304 RQQLDSNLITSEELYMLFPNLGDAIDFQRRFLISLEINALVEPSKQRIQALFMH-SKHF 362
RQ L+++ ++SE++++LFPNL + IDFQRRFL LE N V ORIG++F+H S

40 C.a. Cdc24p: 303 RQDLIEAENLSSEQUIHLFPNLNEIDFQRRFLNGLECNINVPRIYQRIQSVFIHASLGP 362

S.c. Cdc24p: 363 FKLYEPWSIGQNAAEFLSSTLHKMRVDESQRFIINNKLELQSFYKPVQRLCRYPLLVK 422
F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K

45 C.a. Cdc24p: 363 FNAYEPWTIGQLTAIDLINKEAANKKSSS--LLDPGFELQSYILKPIQRLCKYFLLK 419

S.c. Cdc24p: 423 ELLAE-----SSDDNNTKELEAALDISKNARSINENQRRTENHQVVKLYGRV 471
EL+ SS + EL A K +A +NE QRR EN + ++KL RV

50 C.a. Cdc24p: 420 ELIKTSPEYSKQDPHGSSSTSFNELLVAKTAMKELANQVNEAQRRAENIEHLEKLERV 479

S.c. Cdc24p: 472 VNWKGYRISKFGELLYFDKVFISTNSSSEPEREFVYLFEKIILFSEVVTKKSASSLI 531
NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K +

55 C.a. Cdc24p: 480 GNWRGFNLDAQGELLEFGQVGV---KDAENEKEYVAYLFEEKIVFFTEIDDTKKSQKQE 535

S.c. Cdc24p: 532 LKKKSSTASISASNITDNNGSPHHSYHKRHSNSSSSNNIHLSSSSAAAIHSSSTNSSDN 591
K K ST ++SN+ SSS ++ S NS +

60 C.a. Cdc24p: 536 KKSKESTRKRSTSSNL-----SSSTTNLLESINNSRKD 568

S.c. Cdc24p: 592 NSNNSSSSSLFKLSANEPKLDLGRIMIMNLNQIIPQN--NRSINITWESIKEQGNFLK 649
N+ L+L+GR+ I + I N +L I+W KE G+P L+

65 C.a. Cdc24p: 569 NT-----LPLELKGRIYI SEIYNISAPNTPGSTLIISWSCRKESGSFTLR 613

S.c. Cdc24p: 650 FKNEETRDNWSSCLQQLIHLKNEQFKARHSSSTSTSS-----TAKSSMMSPTTT 701
+++EE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T

70 C.a. Cdc24p: 614 YRSEEARNQWEKCLRDCLKTNEMNKQIHKKLRDSDSSEFNTDDSAIYDYTGISTSPVNQSTQ 673

S.c. Cdc24p: 702 MNTPNHNSRQT--HDSMASFSSSHMKRVS----DVLPRKRTTSSSFESIKS----- 748
+H S + H S ++ S RV + TT SF + +

75 C.a. Cdc24p: 674 QQYDHRGSHSSRRHSSSSTLSMMKNRVKSGDLSRISSTSTTLDSFSNNLNGSPNTTNP 733

S.c. Cdc24p: 749 --ISENFKNISIPESILFRISYNNNSNNTSSSEIFILLVEKVVNFDDLIMAINSKI--SN 804
+S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN

80 C.a. Cdc24p: 734 SLMSSDATKTIPTDVAIKLLY---KSTELSE--PLIVNAQIEYNDLLQKIIISQIITSN 787

S.c. Cdc24p: 805 THNNNISPIKIKYQDEGDGDFVVLGSDSDWNVAKEMLAENNEKFLNIRLY 854
++++ I++++Y+D++GDFV L SD+DW + +ML + F +

85 C.a. Cdc24p: 788 LVADDVN--ISRLRYKDEGDGDFVNLNSDDDWGLVLDMLTSED--FYQTSSEKRSVTVVWS 844

Figure 7a

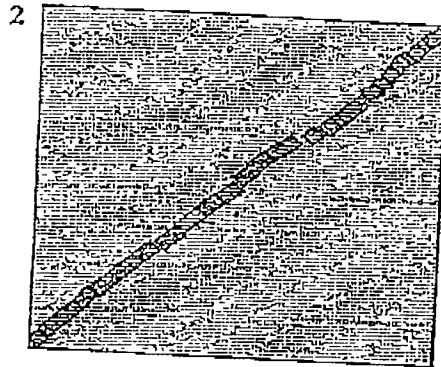
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix: 0.BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☐ Align ☐

Sequence 1 lc|S.c. Cdc24p Length 854 (1..854)

Sequence 2 lc|C.a. Cdc24p Length 844 (1..844)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 446 bits (1136), Expect = e-124

Identities = 288/881 (32%), Positives = 464/881 (51%), Gaps = 112/881 (12%)

```

Query: 9  SGTSLSDLKPKPSATSISIPMQNV--MNKPVTEQDSLPHICANIRKRLVLPQLKPFQL 66
          S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL
Sbjct: 15 STSSLNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEFFLNQ 74

Query: 67 AYQSSEVLSEKQLLSQKQHQELLKSNGANRDSDDLAP---TLRSSSISTATSLMSMEG 123
          A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M
Sbjct: 75 AFNOAEQLSEQQALALAQERSNGNGHNSNGKRHQSLDGAMNRLSVGSDSSSIQGSILTRMAT 134

Query: 124 ISYTNNSNPATPNMEDTLTFSMGILPITMDCDPVTQLSQLFQQGAPLCILFNSVKPQFX 183
          + T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +
Sbjct: 135 NASTSSLISGMPN--NNTLFTFTAGVLPANISVDPATHLWKLFQQGAPFCVLINHILPDSQ 193

Query: 184 LPVIASDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFNSTSQLVKVLEVVEITLMN 243
          +PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+
Sbjct: 194 IPVSSDDLRIKKSVDYDFLIAVKTQLNFDENMFTISNVFSDNAQDLIKIIDVINKLLA 253

Query: 244 SSPTIFPSKSKTQIMNAENQERHQPPQSSKKHNEYVKIIEFVATERKYVHDLEILDKY 303
          S + + + +E K+ +E + TERKYV DLE++ KY
Sbjct: 254 EYSDASDSGGGDEDV-----NMDVQITDERSKVFREIITERKYVQDLELMCKY 302

Query: 304 RQQLDSNLITSEELYMLFPNLGDAIDFORRFLISLEINALVEPSKORIGALFMH-SKHF 362
          RQ L+++ ++SE++++LFFNL + IDFORREL LE N V ORIG++F+H S
Sbjct: 303 RQDLTEAENLSSEQIHLLFPNLNEIIDFORRFLNGLECNINPIRYQRIGSVFIHASLGP 362

Query: 363 FKLYEPWSICQNAAYEFLSSTLHKMRVDESQRFIINNKLELQSFLYKPVQRLCRYPLLVK 422
          F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K
Sbjct: 363 FNAYEPWTIGQLTAIDLINKEAANLKKSSS---LLDPGFELQSYILKPIQLCKYPLLLK 419
  
```


F Figure 7a cont.

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Query: 423 ELLAE-----SSDDNNTKELEAALDISKNIARSINENQRRTENHQVVKKLYGRV 471
 EL+ SS + EL A K +A +NE QRR EN + ++KL RV
 Sbjct: 420 ELIKTSPEYSKODPHGSSSSSTSFNELLVAKTAMKELANQVNEAQRRAENTIEHLEKLERV 479

Query: 472 VNWKGYRISKFGELLYFDKVFISTTNSSSEPEREFVYLFEKIILFSEVVTKKSASSLI 531
 NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K +
 Sbjct: 480 GNWRGFNLDAQGELLFHGQVGV----KDAENEKEYVAYLF EKIVFFFTTEIDDTKKSDKQE 535

Query: 532 LKKKSSTASISASNITDNNGSPHSHYKRRHSNSSSSNNIHLSSSSAAATIHSSSTNSSDN 591
 K K ST ++SN+ SSS ++ S NS +
 Sbjct: 536 KKSSTSTRKSTSSNL-----SSSTTNLLESINNSRKO 568

Query: 592 NSNNSSSSSLFKLSANEPKLDLRGRIMIMNLNQIIPQN--NRSLNITWESIKEQGNFLK 649
 N+ L+L+GR+ I + I N +L I+W KE G+F L+
 Sbjct: 569 NT-----LPLELKGRVYI SEIYNISAPNTPGSTLIISWSCRKESGSPTLR 613

Query: 650 FKNEETRONWSSCLQQLIHDLKNEQFKARHHSSTSTSS-----TAKSSSMMSPPTT 701
 +++2E R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T
 Sbjct: 614 YRSEEARNQWEKCLDLKTNEMNKQIHKLRDSDSSFNTEDDSAIYDYTGISTSPVNQSTQ 673

Query: 702 MNTPNHHNSRQT--HDSMASFSSSHMKRVS----DVLPRKRTTSSSPFESEIKS----- 748
 +H S + H S ++ S RV + TT SF + +
 Sbjct: 674 QQYDHRGSHSSSRHSSSSTLSMMKQNRVKSGDLRSISSTSTTLDSFSNNLNGSPNTTNP 733

Query: 749 --ISENFKNISIPESILFRISYNNNSNNTSSSEIFTLLVEKVWNFDDLIMAINSKI--SN 804
 +S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN
 Sbjct: 734 SLMSSDATKTIPTFDVAIKLLY----KSTELSE--PLIVNAQIEYNDLLQKIISQIITSN 787

Query: 805 THNNNISPIKIKYQDEDDGDFVVLGSDDEDWNVAKEMLAENN 845
 ++++ I++++Y+D++GDFV L SD+DW + +ML +
 Sbjct: 788 LVADDVN-ISRLRYKDDGDFVNLNSDDDWGLVLDMLTSED 827

CPU time: 0.26 user secs. 0.02 sys. secs. 0.28 total secs.

Gapped
 Lambda K H
 0.270 0.0470 0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 12253

Number of Sequences: 0

Number of extensions: 709

Number of successful extensions: 15

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 844

length of database: 90,077,593

effective HSP length: 63

effective length of query: 781

effective length of database: 83353792

effective search space: 65099311552

effective search space used: 65099311552

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 128 (49.9 bits)

X3: 128 (49.9 bits)

S1: 42 (21.9 bits)

S2: 73 (32.8 bits)

Figure 7b

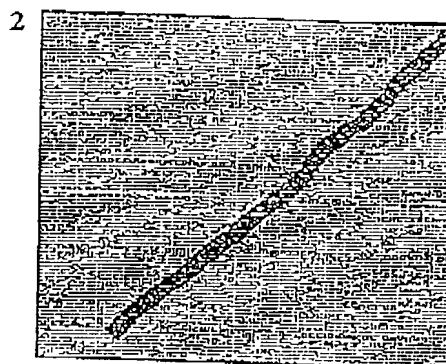
10/24

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix: 0-BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☐ Align

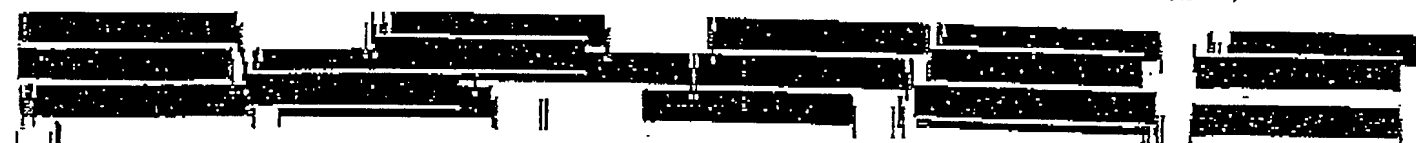
Sequence 1 lcl|S.c. Cdc24p Length 854 (1..854)

Sequence 2 lcl|S.p. Cdc24p Length 834 (1..834)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 238 bits (601), Expect = 1e-61
 Identities = 212/760 (27%), Positives = 348/760 (44%), Gaps = 94/760 (12%)



Query: 156 DPVTQLSQLFQOGAPLCILENSVKPQPKLPVIASDDLK---VCKKSIYDFILGCKKKHFAF 212
 DPVT++ + G PLC LEN + + KL V +S L+ VCK S+Y F+L CK
 Sbjct: 67 DPVTEIWLFCRLGYPLCALFNCLFVKQKLEVNSSVSLENTNVCKASLYRFMLMCKNELGL 126

Query: 213 NDEELFTISDVFANSTSQLVKVLVVETLMNSSPTIFPSKSKTQQIMNAENQERHQPQQS 272
 D LF+IS+++ ST+ LV+ L+ +E L+ +KS + + + S
 Sbjct: 127 TDAALFSISEIYKPPSTAPLVRALQTIELLLKKYEVSNNTTKSSSTPSPSTDDNVPTGTINS 186

Query: 273 SKKHNEYVKIIEFVATERKYVHOLEILDKYRQQLLDSNLITSEELYMLFPNLGDAIDFQ 332
 ++ E TE KY+ DLE L Y L +-+ + + +F NL + +DFQ
 Sbjct: 187 LIASGR--RVTAEIYETELKYIQDLEYLSNYMVILQQKQILSQDTILSIFTNLNEILDFO 244

Query: 333 RRFLISLEINALVEPSKQRIGALFMHSHKHFPLYEPWSIG-QNAAIEFLSSTLHKMRVDE 391
 RRFL+ LE+N + +QR+GALF+ + F +Y+ + .NA + + ++V
 Sbjct: 245 RRFLVGLEMNLSLPVEEQRLCALFIALEEGFSVYQVFCNTNFPNAQQLIIDNQQLLKVAN 304

Query: 392 SQRFIINNKLQSFYLYKPVQRLCRYPLLKELL-AESSDDNNTKELEAALDISKNIARS 450
 ++ EL + L KP+QR+C+YPLL+ +LL S +EL+ + +A
 Sbjct: 305 ----LLEPSYELPALLIKPIQRICKYPLLNLQLLKGTTPSGYQYEEELKQGMACVVRVANQ 360

Query: 451 INENQRRRTENHQVVKLYGRVWNWKGYSKFGELLYFDKVPFISTNNSSEPEREFEVYL 510
 +NE +R EN + +L RV++WKGY + FG+LL +D V + ++ ERE+ VYL
 Sbjct: 361 VNETARRIHENRNAIIELEQRVIDWKGYSLOQYFGQLLVWDVVNV----CKADIEREYHVYL 416

Query: 511 FEKIIILPSEVVT-KKSASSLILKKKSSTAS-----ISASNITDN----- 550
 FEKI++ E+ T K+ A S+ + KK+ S I SNIT
 Sbjct: 417 FEKILLCKEMSTLKROARSISMNKKTKRLDSLQKGRILTSNITTVPNNHMGSYAIOI 476

Figure 7b cont..

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Query: 551 --NGSPHHSYHKRHSNSSSSNNIHL-----SSSAAAIHSSTNSSDNNNSNNSSSS 599
 G P H + S+ + +S + I S+ ++ N N SSS
 Sbjct: 477 FWRGDPQHESFILKLRNEESHKLWMSVLNRLWLKNEHGSFKDIRSAASTPANPVYNRSS 536

Query: 600 SLFKLSANEPKLD-LRGRIMIMNLN---QIIPQNNRSLNITWESIKEQGNFLLKPKNEET 655
 K N D LR + N+N I +++S T + K+ K+ T
 Sbjct: 537 QTSK-GYNSSDYDLLRTHSLDENVNSPTSISSPSKSSPFTKTTSKDT-----KSATT 588

Query: 656 RDNWSSCLOQLIHDLKNEQFKARHHSSTST-----TSSTAKSSSMMSPPTTMTNT--PNHH 708
 D S +L + R +TST +SSTA S +S + +N+ +++
 Sbjct: 589 TDERPSDFIRLNSEESVGTSSLRTSQTSTIVSNDSSSTASIPSQISRISQVNSLLNDYN 648

Query: 709 NSRQTH-----DSMASF---SSSHMKRVSD-----VLPKRRTTSSSPFESE 745
 +RQ+H S++ F SSS +++ D + P++ + S+ +S+
 Sbjct: 649 YNRQSHITRVYSGTDDGSSVSIFEDTSSSTKQKIFDQPTTNDCDVMRPRQYSYSAGMKSD 708

Query: 746 IKSISENFKNSIPESSILFRISYNNNSNNTSSSEI---FTLLVEKVWNFDDLLIMAINSK 801
 + S+ SS +S N +N + L+V FD+L+ + K
 Sbjct: 709 GSLLPSTKHTSLSSSSTSTSLSVRNTTNVKIRLRLEHVSLLVVAHDITFDELLAKVERK 768

Query: 802 IS--NTHNNNISPIKIKYQDEGDGFVVLGSDDEDWNVAKE 839
 I + ++KY DEDGDF+ + SDED +A E
 Sbjct: 769 IKLCGILKQAVPFRVRLKYVDEGDGFITITSDVDVLMFAE 808

CPU time: 0.26 user secs. 0.04 sys. secs 0.30 total secs.

Gapped
 Lambda K H
 0.270 0.0470 0.230

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 10384
 Number of Sequences: 0
 Number of extensions: 671
 Number of successful extensions: 13
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 2
 Length of query: 834
 Length of database: 90,077,593
 effective HSP length: 61
 effective length of query: 773
 effective length of database: 83489227
 effective search space: 64537172471
 effective search space used: 64537172471
 T: 9
 A: 40
 X1: 16 (7.3 bits)
 X2: 128 (49.9 bits)
 X3: 128 (49.9 bits)
 S1: 41 (21.7 bits)
 S2: 73 (32.8 bits)

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Figure 8

5 Sc KLPVIASDDLKVCKKSIYDFIL (SEQ ID No 25)

++PV++SDDL++CKKS+YDF++

Ca QIPVVSSDDLRLCKKSVYDFLI (SEQ ID No 26)

10 Sc = *Saccharomyces cerevisiae*

Ca = *Candida albicans*

A

Fungal Cdc24's

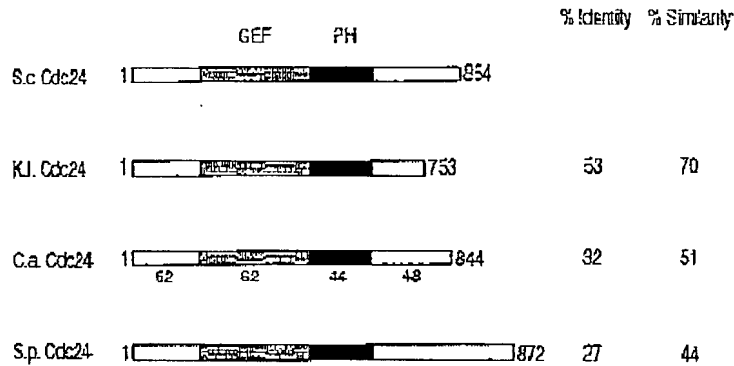


figure 9

B

Guanine nucleotide exchange factor domain of CaCDC24 is homologous to other fungal Cdc24p's

S.c.	227	SGGCAVYVGVVAVPSSSTPTPEINRTCCQMAKFWQRHQPQSSKKNINENVQETINEN
K.l.	232	SGDHPEKVLADVNTLENAAPVPEOLDNSTRLEW-----S-GRVAKPQTEINENVQETINEN
C.a.	237	NAQDLEITIDVINEELAEVSDASDGGGDDVDN-----MDVQETIDERSVVFRET
S.p.	179	STAPFEVRAEQTIEMHKKKVEVSNNTTSSSPSPSTDDN--VPTGTINENSLASGRRTVETEL
S.c.	287	VAETIRYVYVHDSYDCKNSDPAESSTETZLIPVHMSSTIGDALCFQSSALVHPCVSAIT
K.l.	272	VEIERAVVQVYVHDSYDCKNSDPAESSTETZLIPVHMSSTIGDALCFQSSALVHPCVSAIT
C.a.	286	VEIERAVVQVYVHDSYDCKNSDPAESSTETZLIPVHMSSTIGDALCFQSSALVHPCVSAIT
S.p.	177	VAETIRYVYVHDSYDCKNSDPAESSTETZLIPVHMSSTIGDALCFQSSALVHPCVSAIT
S.c.	347	SHKERRALPPEHRE-PELVPEADSLGQVNSHPURSTFLWVVDGQSTYANQILINQ
K.l.	332	SGDHPEKVLADVNTLENAAPVPEOLDNSTRLEW-----S-GRVAKPQTEINENVQETINEN
C.a.	344	THVAKPGQVHDAVLGPNVINEELAEVSDASDGGGDDVDN-----MDVQETIDERSVVFRET
S.p.	297	VAETIRYVYVHDSYDCKNSDPAESSTETZLIPVHMSSTIGDALCFQSSALVHPCVSAIT
S.c.	405	SHKERRALPPEHRE-PELVPEADSLGQVNSHPURSTFLWVVDGQSTYANQILINQ
K.l.	390	SGDHPEKVLADVNTLENAAPVPEOLDNSTRLEW-----S-GRVAKPQTEINENVQETINEN
C.a.	403	THVAKPGQVHDAVLGPNVINEELAEVSDASDGGGDDVDN-----MDVQETIDERSVVFRET
S.p.	153	VAETIRYVYVHDSYDCKNSDPAESSTETZLIPVHMSSTIGDALCFQSSALVHPCVSAIT
S.c.	455	SHKERRALPPEHRE-PELVPEADSLGQVNSHPURSTFLWVVDGQSTYANQILINQ
K.l.	439	SGDHPEKVLADVNTLENAAPVPEOLDNSTRLEW-----S-GRVAKPQTEINENVQETINEN
C.a.	463	THVAKPGQVHDAVLGPNVINEELAEVSDASDGGGDDVDN-----MDVQETIDERSVVFRET
S.p.	403	VAETIRYVYVHDSYDCKNSDPAESSTETZLIPVHMSSTIGDALCFQSSALVHPCVSAIT

C

Homology of Ste4p binding region

S.c.	170	PLCILFNSVKKPQFELPTVNSDDEK---VCKKSIYDETLGCKVHVFENDEELSTISDVFN
K.l.	164	PLCILFNSVKKPQFELPTVNSDDEK---VCKKSIYDETLGCKVHVFENDEELSTISDVFN
C.a.	180	PLCILFNSVKKPQFELPTVNSDDEK---VCKKSIYDETLGCKVHVFENDEELSTISDVFN
S.p.	115	PLCILFNSVKKPQFELPTVNSDDEK---VCKKSIYDETLGCKVHVFENDEELSTISDVFN
S.c.	227	SGGCAVYVGVVAVPSSSTPTPEINRTCCQMAKFWQRHQPQSSKKNINENVQETINEN
K.l.	221	SGDHPEKVLADVNTLENAAPVPEOLDNSTRLEW-----S-GRVAKPQTEINENVQETINEN
C.a.	237	NAQDLEITIDVINEELAEVSDASDGGGDDVDN-----MDVQETIDERSVVFRET
S.p.	179	STAPFEVRAEQTIEMHKKKVEVSNNTTSSSPSPSTDDN--VPTGTINENSLASGRRTVETEL

D

Homology of Bem1p binding region

S.c.	774	-----NLSSEIRFVAVYKVVNFDEIKANSGEISNTHMNI-S-PLVKKVAVQ
K.l.	789	-----DFVYVYVYSLCSAEDEELAKREABLE-----VIRKVVAVQ
C.a.	746	TPD--VAITELVYKSTELSEPLINNACTEYNOLLQRTISQITTSNTVADD--NLSKREVEE
S.p.	768	SVANTNVVITRLALSEVGLVGVVAHDTTELEELAKVSEELKLCSTDRQAMPFVAVLV
S.c.	822	EDGDDVYVYVYKVVNFDEIKANSGEISNTHMNI-S-PLVKKVAVQ
K.l.	723	EDGDDVYVYVYKVVNFDEIKANSGEISNTHMNI-S-PLVKKVAVQ
C.a.	804	EDGDDVYVYVYKVVNFDEIKANSGEISNTHMNI-S-PLVKKVAVQ
S.p.	828	EDGDDVYVYVYKVVNFDEIKANSGEISNTHMNI-S-PLVKKVAVQ

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Figure 10

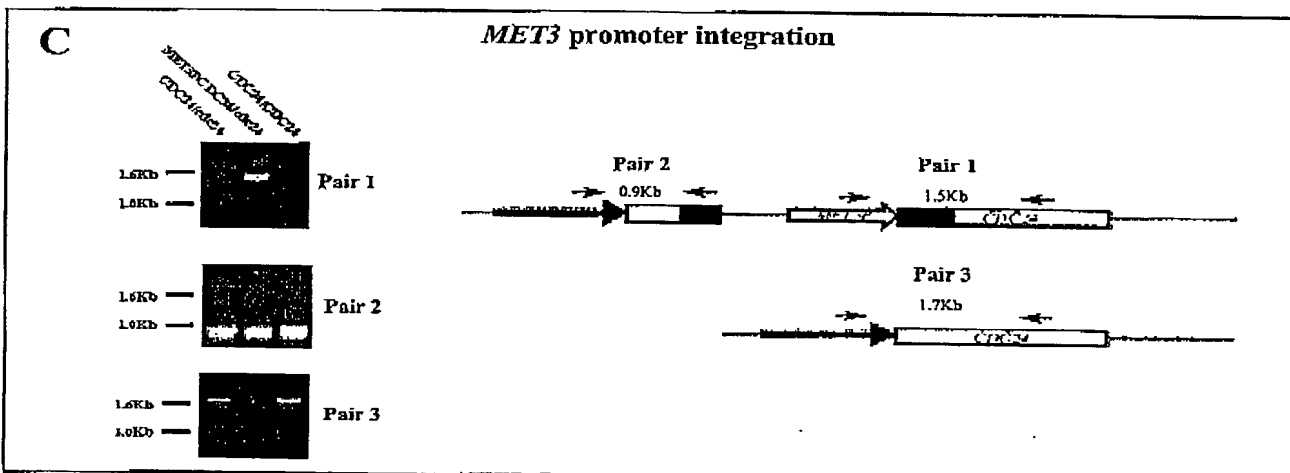
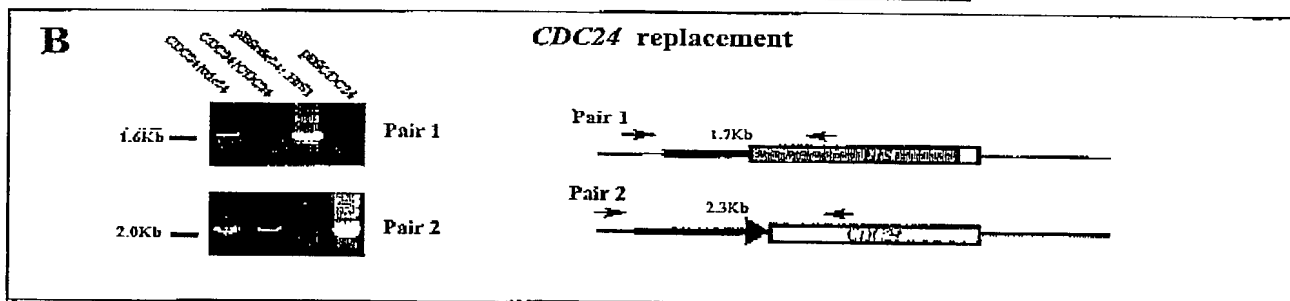
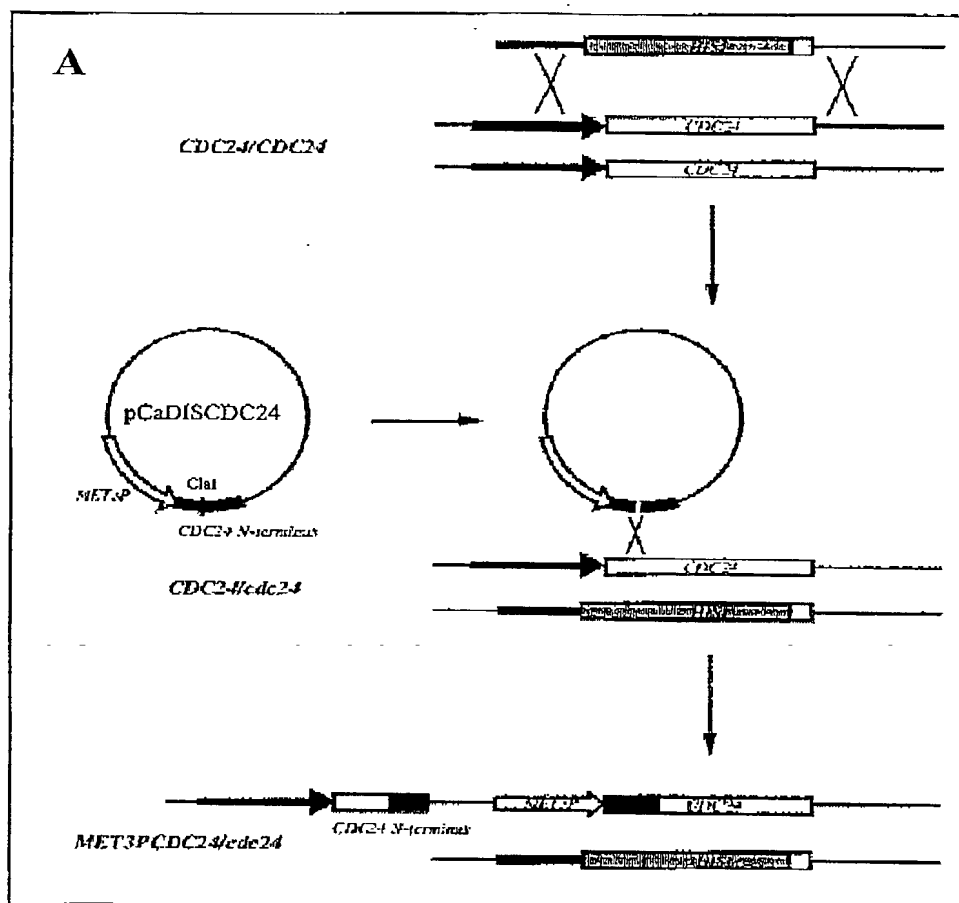
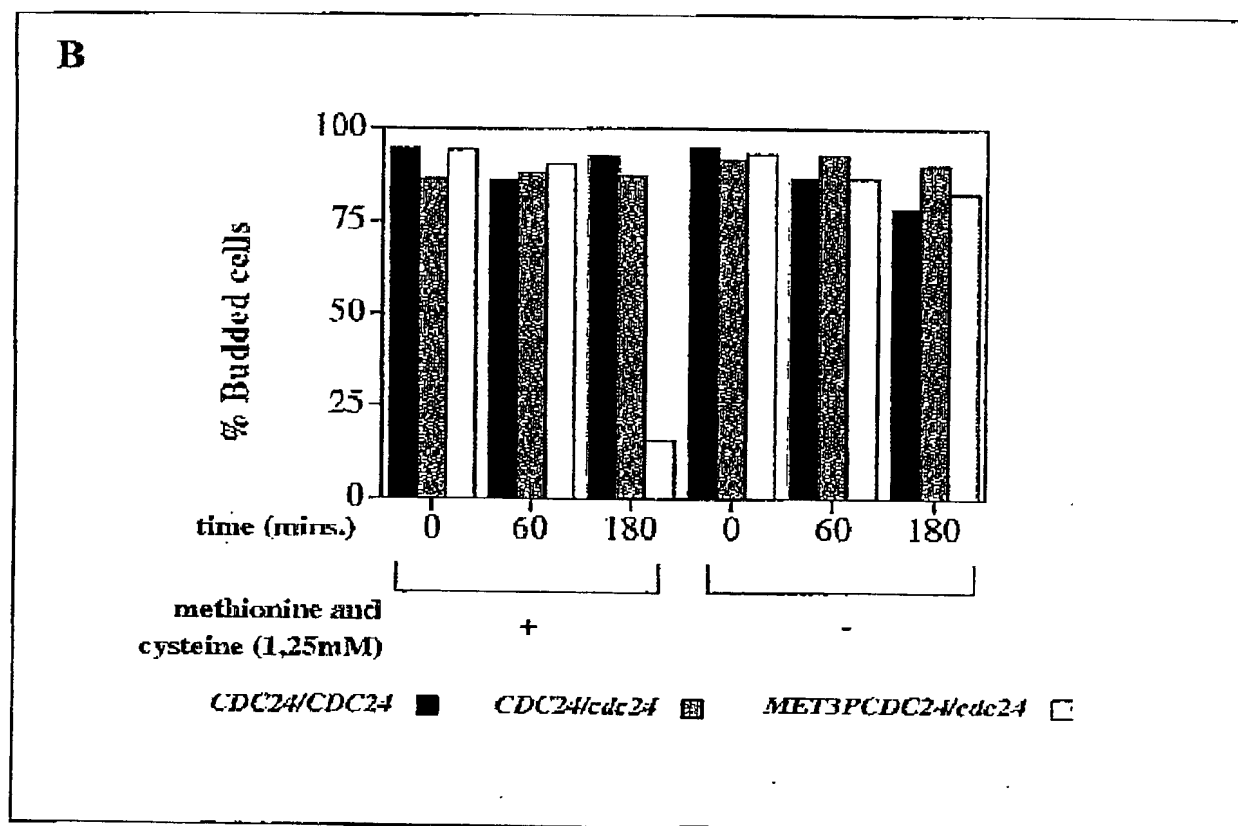
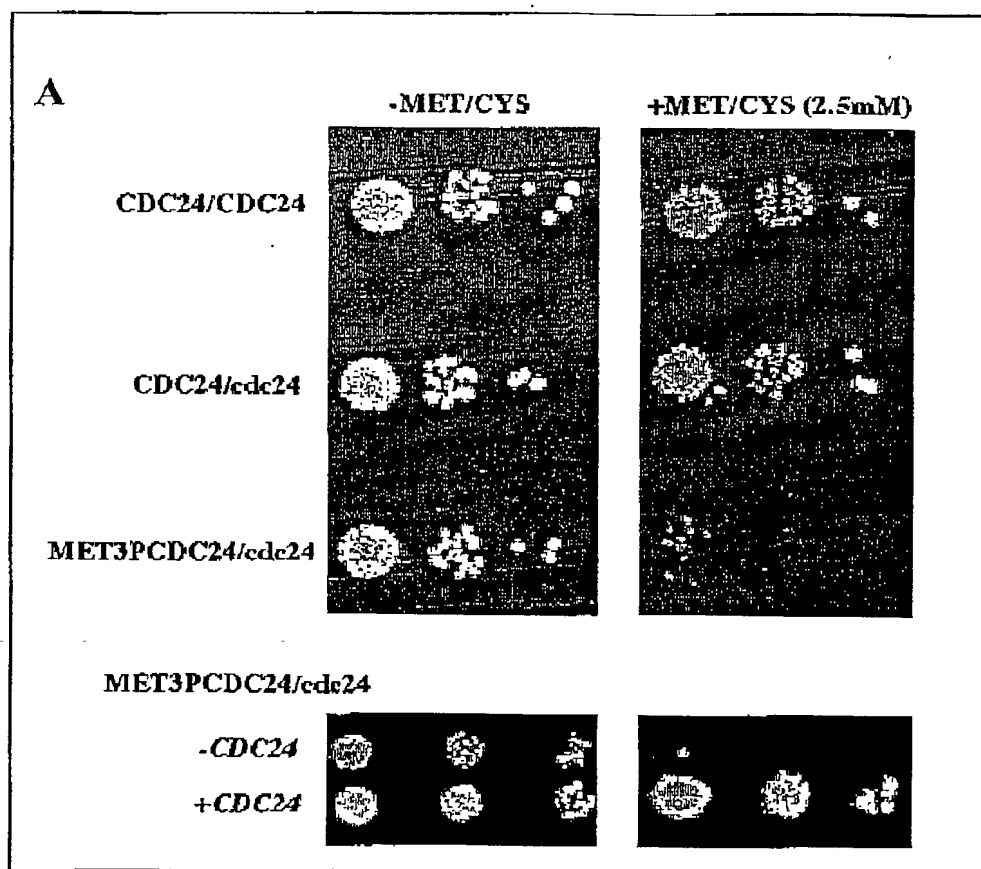


Figure 11



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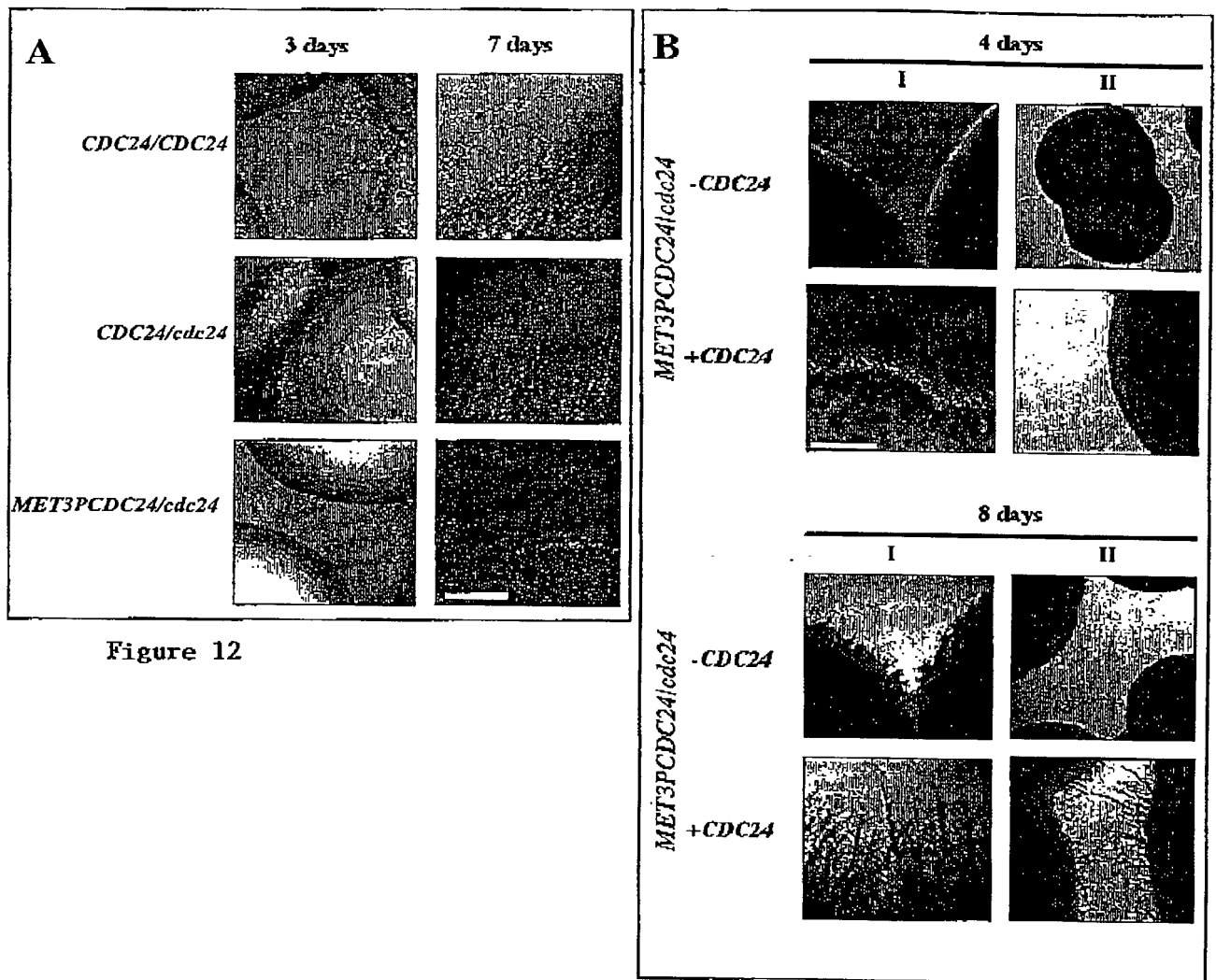


Figure 12

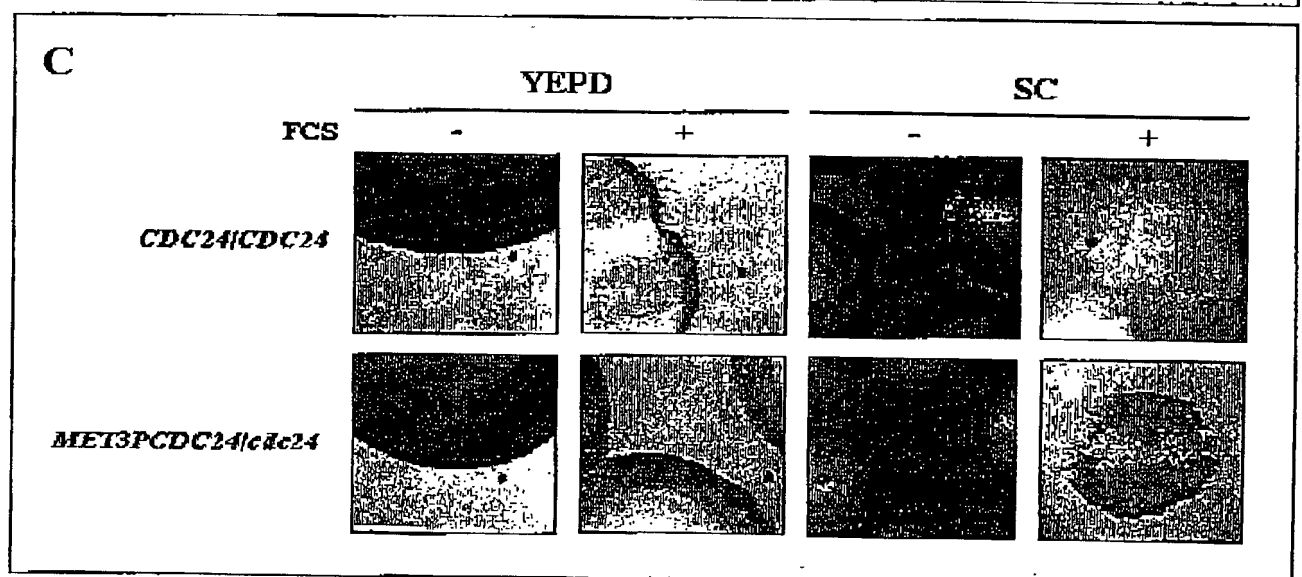


Figure 13

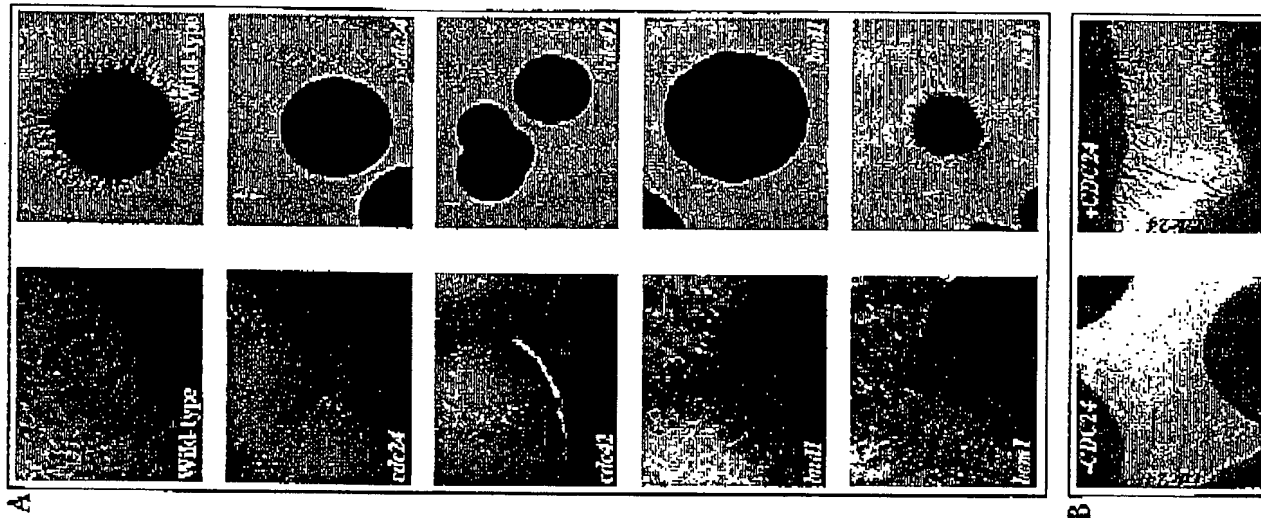
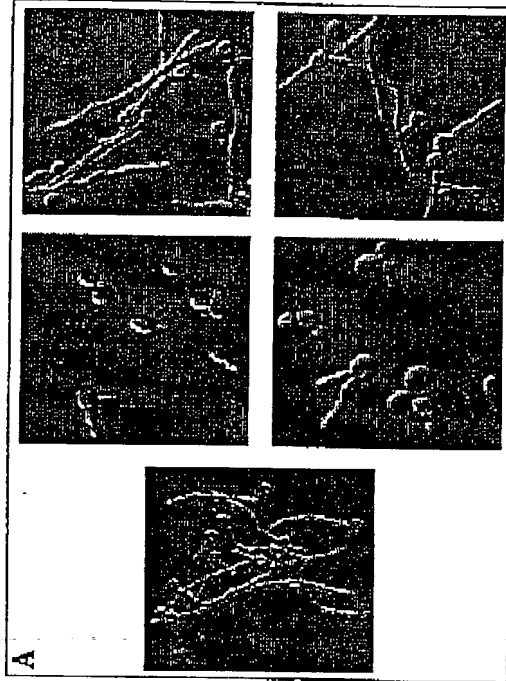
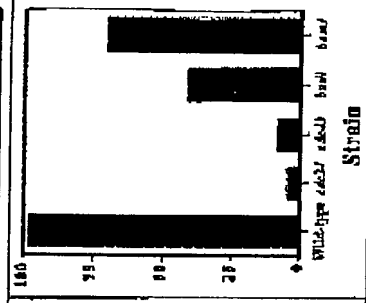


Figure 14B



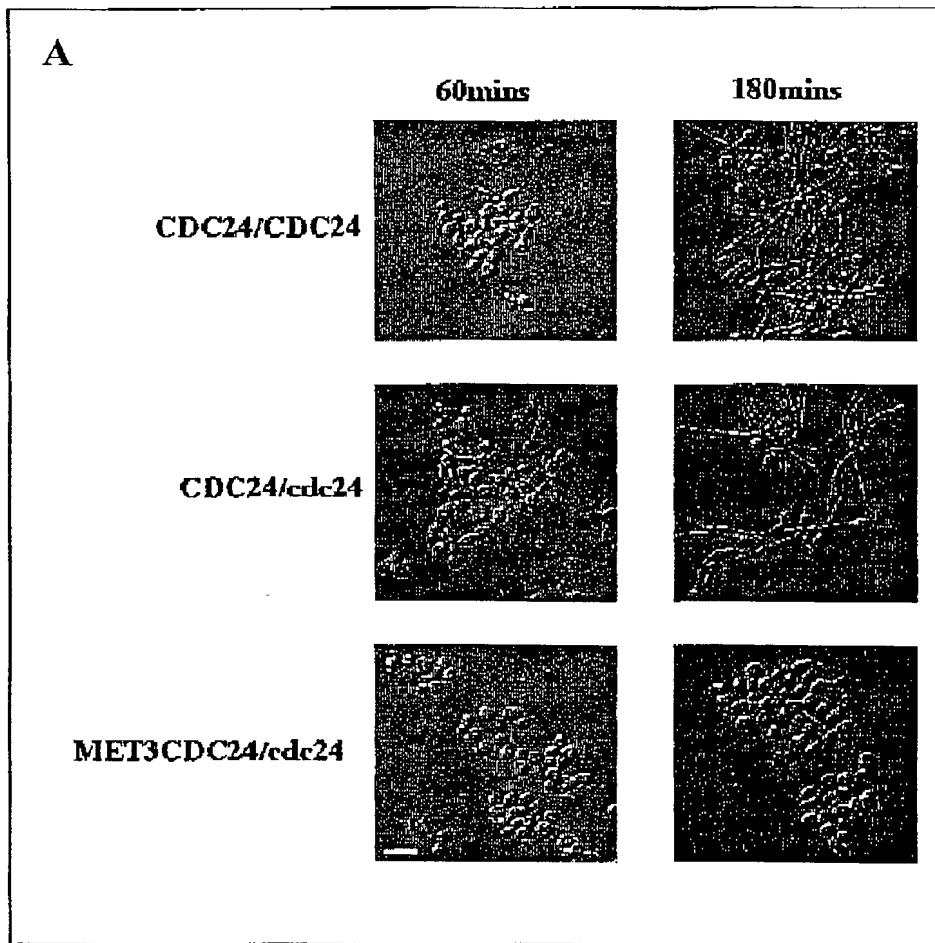


Figure 15

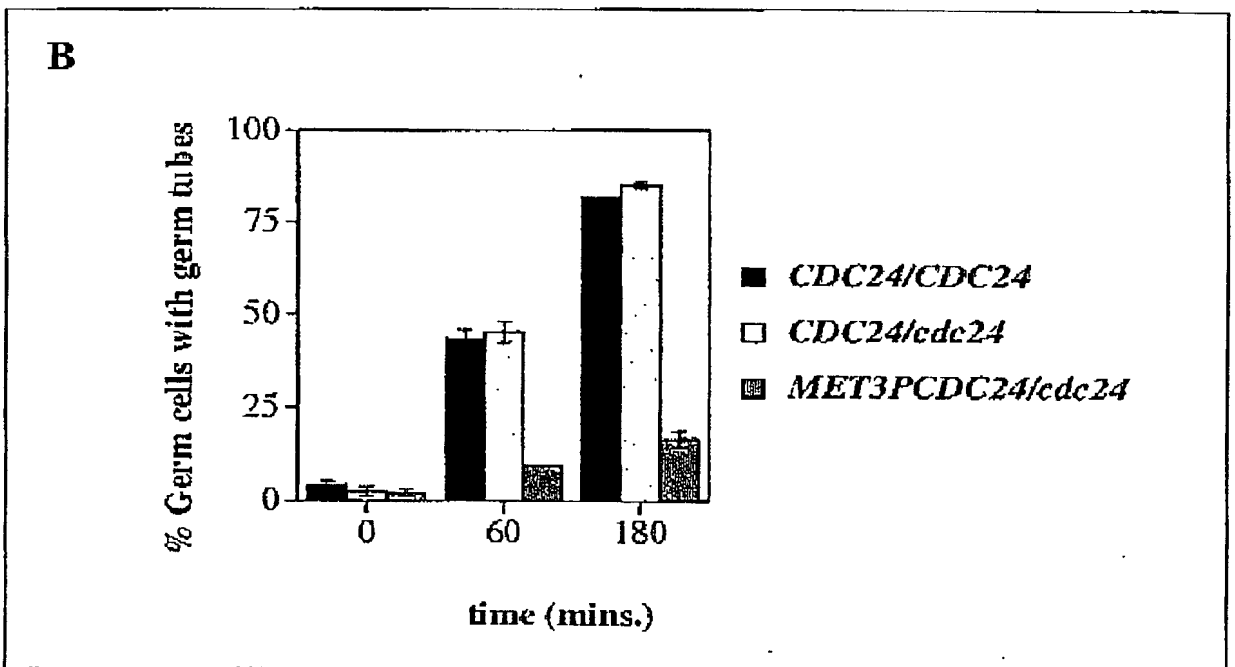
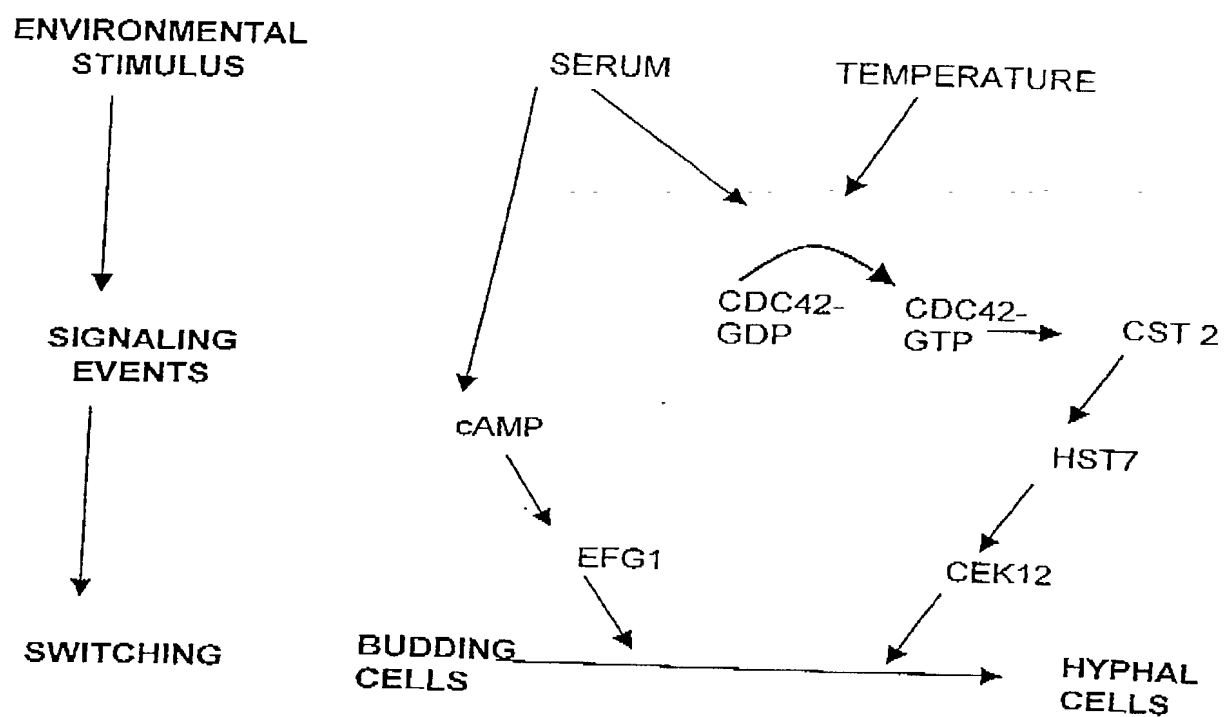


Figure 16



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Figure 17

A. *cdc24* (wt)

5

SEQ. I.D. NO:1

DNA:

ccccctgtatactttcaactctgtgaagccgcaatttaaattaccggaatagcatctgacgatttgaaagtctgtaaaaatccattatgactt
10 tatattgggctgcaagaaacactttgcatttaacgatgaggagcttttactatatccgacgttttgccaactcgacgtcccagctggtaaagt
gctagaagtagtagaaacgctaataatgaattccagc

SEQ. I.D. NO:2

Protein:

15 PLCILFNSVKPQFKLPVIASDDLKVCKKSIYDFILGCKKHFANDEELFTISDVFANSTSQ
LVKVLEVVEITLMNSS

B. *cdc24-m1*

20 SEQ. I.D. NO:3

DNA:

ccccctgtatactttcaactctgtgaagccgcaatttaaattaccggaatagcattgacgatttgaaagtctgtaaaaatccattatgacttt
atatgggctgcaagaaacactttgcatttaacgatgaggagcttttactatatccgacgttttgccaactcgacgtcccagctggtaaagt
gctagaagtagtagaaacgctaataatgaattccagc

25

SEQ. I.D. NO:4

Protein:

PLCILFNSVKPQFKLPVIAFDDLKVCKKSIYDFILGCKKHFANDEELFTISDVFANSTSQ
LVKVLEVVEITLMNSS

30

C. *cdc24-m2*

5 SEQ. I.D. NO:5

DNA:

cccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcatctggcgatttgaaagtctgtaaaaatccatttatgactt
tatattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

10

SEQ. I.D. NO:6

Protein:

PLCILFNSVKPQFKLPVIASGDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEV VETLMNSS

15

D. *cdc24-m3*

SEQ. I.D. NO:7

DNA:

20 cccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcacctgacgatttgaaagtctgtaaaaatccatttatgactt
tatattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

SEQ. I.D. NO:8

25 Protein:

PLCILFNSVKPQFKLPVIAPDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEV VETLMNSS

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SEQ ID NO. 10

STE4 DNA sequence (wild-type)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCACAGTATATACACCCACAAAGTCTACAGGA
 TATCTCTGCAGTGGAGGAGAAATTCAAATAAATATAGAGGCCGCCAGACAGAGAGTAAACAGCTTCATGCTCAATAA
 ATTAAGCAAAATACAGATACAGATGCAAGCTTATTCAGATGGCCACAAAGTTACTTCGTTGACCAAAATAAGATC
 5 AACTTAAGCCAAATATCGTGTGAAAGGCCATAATAATAAATCTCAGATTTTCGGTGGAGTCCAGATTCAAACGTAT
 TTTGAGTGCAGTCAAGTGGCTTTAIGCTTATATGGGACAGTGCCTTCAGGTTTAAACAGACACGCTATTCATTAGATT
 CTCATGGGTTCTTTCCCTGCGCTATTTCCGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAAACAATAACTGTACCATT
 TATAGAGTTTTCGAAAGAAACAGAGTAGCGCAAPACGTTGCGTCAATTTCAAAGGACATACTTGCTATATTTCTGACAT
 TCAATTTACAGATACGCAATATATTGACAGCAAGTGGGGATATGACATGTGCCCTGTGGGATATACCGAAAGCAAAGA
 10 GGGTGAGAGATATTTCTGACCATTTAGGTGATGTTTTGGCATTAGCTATTCCTGAAGAGCCAACTTAGAABATTCCTCG
 AACACATTGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCCTCCCTGTACAAAGCTTTTA
 CGTTAACGATATGATATTAATGCACTTCGTTTCTTCAAAAGCTGCTGCTATTTCTGAGGATTTGAAAGCTATCCCTTCC
 TAAATATGATATGATTAAGGTGGGACTGTTCTATGCTACTTTCTCTCTTTTCGAGGTTATGAAAGCTATCCCTTCC
 CCTACTTATATGCGAGCTAATGAGTACAATAACCGCGCAATCGCCACAACTTTAAATCAACAGCTCAAGCTATCT
 15 AACACAAACAAAGGCTGTTCTTTAGATTTTATGTCATCTGGAAGATTGATGTAATCATGCTATACAGACATTGCTGCTG
 TTCTGTGGGATCTATTAAGGAGAGATTGTTGGAATATTAGAAAGTCTATGGTGGCAGAGTCACTGGTGTGCGCTCGAGT
 CCAGATGGGTTAGCTGATGACAGGTTTCATGGGACTCAACCATGAAATATGCTCTCCAGGTTATCAATAG

20

SEQ ID NO. 11

Ste4 Protein sequence (wild-type)

MAHQMDSITYSNVTCQYIQPQSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFOMANKVTSLTKNKEI
 LKPNIVLKGENNAISDFRWSRDSKRILSASQDGFMLIWDASGLKQNAIFLDSQVWLSCAISPSTLIVASAGLNMNCTI
 25 FVSKENRVAQWVASIFKHTCYISDIEFTDNAHILTASGDMTCALWDIPKAKRVREYSOHLGCVLALATFEENLENS
 TFASCGSDGYTYINDERSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGATNMYDLRSDCSIAITFSLFRGYEERTPT
 TYMAANMEYNTRQSPQELKSTSSSYLDNQGVVSLDFSASGRLMYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVRES
 EGLAVCTGSWDSTMKIWSPGYQ

30

SEQ ID NO. 12

ste4-o15 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCACAGTATATACACCCACAAAGTCTACAGGA
 35 TATCTCTGCAGTGGAGGAGAAATTCAAATAAATATAGAGGCCGCCAGACAGAGAGTAAACAGCTTCATGCTCAATTA
 ATTAAGCAAAATACAGATACAGATGCAAGCTTATTCAGATGGCCACAAAGTTACTTCGTTGACCAAAATAAGAT
 AACTTAAGCCAAATATCGTGTGAAAGGCCATAATAATAAATCTCAGATTTTCGGTGGAGTCCAGATTCAAACGT

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TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCTTCAGGTTTAAACAGAACGCTATTCCATTAGAI
 CTCAATGGGTTCTTTCTGCGCTATTTTCGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAACCAATAACTGTACCAI
 TATAGAGTTTTCGAAAGAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAAGGACATACTTGGTATATTTCTGACA
 TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAG
 5 GGGTGAGAGGATATTCTGACCATTAGGTGATGTTTTGGCATTAGCTATTCCCTGAAGAGCCAACTTAGAAAATTCTTC
 AACACATTTCGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCGCTGTACAAAGCTTTT
 CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTCAAAGACGGGATGTCGATTGTTGCAGGAAGTGACAATGGTGCG
 TAAATATGTATGATTTAAGGTGCGACTGTTCTATTGCTACTTTTTCTCTTTTCGAGGTTATGAAGAACGTACCCCTAC
 CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATCGCCACAACTTTAAATCAACAGCTCAAGCTATC
 10 AGACAACCAAGGCGTTGTTTTCTTTAGATTTTAGTGATCTGGAAGATTGATGTACTCATGCTATACAGACATTGGTTGT
 TTGTGTGGGATCTATTAAAGGAGAGATTGTTGGAAAATTAGAAGGTCATGGTGGCAGAGTCACTGGTGTGCGCTCGAG
 CCAGATCGGCTAGCTTATCTACAGGTTGATGGGACTCAACCATGAATATATGGTCTCCAGGCTATCAATG

SEQ ID No. 13

15 Ste4-o15 Protein sequence (mutant)

MAHQMDSTYTSNNVTQQYIQPQSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNK
 LKPNIVLKGNHNNKISDFRWSRDSKRILSASQDGFMLIWDASGLKQNAIPLDSQWVLSCAISPSSTLVASAGLNNCT
 RVSKENRVAQNVAIFKGHTCYISDIEFTDNAHILTAGDMTCALWDIPKAKRVRGYSOHLGQVLAALAIPEEPNLENS
 20 TFASCGSDGYTYIWDSSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTF
 TYMAANMEYNATAQSPQTLKSTSSSYLONQGVVSLDPSASGRMLMYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVRS:
 DGLAVCTGSWDSTMKIWSPGYQ

SEQ ID NO. 14

25 ste4-o17 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATATACAACCACAAAGTCTACAGGA
 TATCTCTGCAGTGGAGGAAGAAATTCAAATAAATAGAGGCCGCCAGACAAGAGAGTAACAGCTTCATGCTCAAATP
 ATAAGCAAAACACAAGATACAAGATGCAAGCTTATTCCAGATGGCCACAAAGTTACTTCGTTGACCAAAAATAAGAI
 30 AACTTAAAGCCAAATATCGTGTTGAAAGGCCATAATAATAAATCTCAGATTTTCGGTGGAGTGGAGATTCAAACGTA
 TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCTTCAGGTTTAAACAGAACGCTATTCCATTAGAI
 CTCAATGGGTTCTTTCTGCGCTATTTTCGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAACCAATAACTGTACCAI
 TATAGAGTTTTCGAAAGAAACAGAGTAGCGCAAAACGTTGCGTCAATTTCAAAGGACATACTTGGTATATTTCTGACA
 TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAG
 35 GGGTGAGAGGATATTCTGACCATTAGGTGATGTTTTGGCATTAGCTATTCCCTGAAGAGCCAACTTAGAAAATTCTTC
 AACACATTTCGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCGCTGTACAAAGCTTTT
 CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTCAAAGACGGGATGTCGATTGTTGCAGGAAGTGACAATGGTGCG

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TAAATATGTATGATTTAAGGTCGGACTGTTCTATTGCTACTTTTTCTCTTTTCGAGGTTATGAAGAACGTACCCCTACC
 CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATCGCCACAAACTTTAAAATCAACAGCTCAAGCTATCT
 AGACAACCAAGGCGCTGTTTCTTTAGATTTTAGTGCACTCTGGAAGATTGATGTACTCATGCTATACAGACATTGGTTGTG
 TTGTGTGGGATGTATTAAAGGAGAGATTGTTGGAAAATTAGAAGGTCATGGTGCCAGAGTCACTGGTGTGCGCTCGAGT
 5 CCAGATGGGTTAGCTGTATGTACAGGTCATGGGACTCAACCATGAAATATGGTCTCCAGGTTATCAATAG

SEQ ID No. 15

Ste4-o17 Protein sequence (mutant)

10 MAHQMDSITYSNNVTQQYIQPSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNKI
 LKPNIVLKGHNKISDFRWSRDSKRILSASQDGFMLIWDSASGLKQNAIFLDSQWVLSCAISPSSTLVASAGLNNNCTT
 RVSKENRVAQNVAIFKGHTCYISDIEFTDNAHILTAGDMTCALWDIPKAKRVREYSQHLGDLALAIPEEPNLENSI
 TFASCGSDGYTYIWDSRSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYERTPT
 TYMAANMEYNTAQSPQTLKSTSSSYLDNQGAVSLDFSASGRMLMYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVASE
 15 DGLAVCTGSWDSTMKIWSFGYQ

SEQ. I.D. No:16 refers to the epitope sequence "Tyr Pro Tyr Asp Val Pro Asp Tyr Ala".

SEQ. I.D. No:17 refers to TEV protease recognition sequence "Gln Asn Leu Tyr Phe Gln Gly"

SEQ. I.D. No:18 refers to peptide sequence "QFKLPVIAFDDLKVCKKSI".

SEQ. I.D. No:19 refers to peptide sequence "QFKLPVIASGDLKVCKKSI".

SEQ. I.D. No:20 refers to peptide sequence "QFKLPVIAPDDLKVCKKSI".

SEQ. I.D. No:21 refers to peptide sequence "QFKLPVIASDDLKVCKKSI".

SEQ. I.D. No:22 refers to peptide sequence "QYEFDVILSPELKVQMKT".